

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/526,207

Source: P4/10

Date Processed by STIC: 3/16/05

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PCT

RAW SEQUENCE LISTING

DATE: 03/16/2005

PATENT APPLICATION: US/10/526,207

TIME: 08:22:19

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03162005\J526207.raw

3 <110> APPLICANT: BASF Aktiengesellschaft

5 <120> TITLE OF INVENTION: GTP-Cyclohydrolase II as a target for fungicides

7 <130> FILE REFERENCE: 20020217

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/526,207

C--> 10 <141> CURRENT FILING DATE: 2005-03-04

12 <160> NUMBER OF SEQ ID NOS: 5

14 <170> SOFTWARE: PatentIn Ver. 2.1

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 903

18 <212> TYPE: DNA

19 <213> ORGANISM: Ashbya gossipii

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (1)..(903)

25 <400> SEQUENCE: 1

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28 1 5 10 15
30 ata ccg acg gta cag ggc acc gat gtc ttc ctc cat cta tac cac aac 96
31 Ile Pro Thr Val Gln Gly Thr Asp Val Phe Leu His Leu Tyr His Asn
32 20 25 30
34 tcg atc gac agc aag gaa cac cta gcg att gtc ttc ggc gag aac ata 144
35 Ser Ile Asp Ser Lys Glu His Leu Ala Ile Val Phe Gly Glu Asn Ile
36 35 40 45
38 cgc tcg cgg agt ctg ttc cgg tac cgg aaa gac gac acg cag cag gcg 192
39 Arg Ser Arg Ser Leu Phe Arg Tyr Arg Lys Asp Asp Thr Gln Gln Ala
40 50 55 60
42 cgg atg gtg cgg ggc gcc tac gtg ggc cag ctg tac ccc ggg cgg acc 240
43 Arg Met Val Arg Gly Ala Tyr Val Gly Gln Leu Tyr Pro Gly Arg Thr
44 65 70 75 80
46 gag gca gac gcg gat cgg cgt cag ggc ctg gag ctg cgg ttt gat gag 288
47 Glu Ala Asp Ala Asp Arg Arg Gln Gly Leu Glu Leu Arg Phe Asp Glu
48 85 90 95
50 aca ggg cag ctg gtg gtg gag cgg gcg acg acg tgg acc agg gag ccg 336
51 Thr Gly Gln Leu Val Val Glu Arg Ala Thr Thr Trp Thr Arg Glu Pro
52 100 105 110
54 aca ctg gtg cgg ctg cac tcg gag tgt tac acg ggc gag acg gcg tgg 384
55 Thr Leu Val Arg Leu His Ser Glu Cys Tyr Thr Gly Glu Thr Ala Trp
56 115 120 125
58 agc gcg cgg tgc gac tgc ggg gag cag ttc gac cag gcg ggt aag ctg 432
59 Ser Ala Arg Cys Asp Cys Gly Glu Gln Phe Asp Gln Ala Gly Lys Leu
60 130 135 140
62 atg gct gcg gcg aca gag ggc gag gtg gtt ggc ggt gcg ggg cac ggc 480

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63 Met Ala Ala Ala Thr Glu Gly Glu Val Val Gly Gly Ala Gly His Gly
64 145                      150                      155                      160
66 gtg atc gtg tac ctg cgg cag gag ggc cgc ggc atc ggg cta ggc gag 528
67 Val Ile Val Tyr Leu Arg Gln Glu Gly Arg Gly Ile Gly Leu Gly Glu
68                      165                      170                      175
70 aag ctg aag gcg tac aac ctg cag gac ctg ggc gcg gac acg gtg cag 576
71 Lys Leu Lys Ala Tyr Asn Leu Gln Asp Leu Gly Ala Asp Thr Val Gln
72                      180                      185                      190
74 gcg aac gag ctg ctc aac cac cct gcg gac gcg cgc gac ttc tcg ttg 624
75 Ala Asn Glu Leu Leu Asn His Pro Ala Asp Ala Arg Asp Phe Ser Leu
76                      195                      200                      205
78 ggg cgc gca atc cta ctg gac ctc ggt atc gag gac atc cgg ttg ctc 672
79 Gly Arg Ala Ile Leu Leu Asp Leu Gly Ile Glu Asp Ile Arg Leu Leu
80                      210                      215                      220
82 acg aat aac ccc gac aag gtg cag cag gtg cac tgt ccg ccg gcg cta 720
83 Thr Asn Asn Pro Asp Lys Val Gln Gln Val His Cys Pro Pro Ala Leu
84 225                      230                      235                      240
86 cgc tgc atc gag cgg gtg ccc atg gtg ccg ctt tca tgg act cag ccc 768
87 Arg Cys Ile Glu Arg Val Pro Met Val Pro Leu Ser Trp Thr Gln Pro
88                      245                      250                      255
90 aca cag ggc gtg cgc tcg cgc gag ctg gac ggc tac ctg cgc gcc aag 816
91 Thr Gln Gly Val Arg Ser Arg Glu Leu Asp Gly Tyr Leu Arg Ala Lys
92                      260                      265                      270
94 gtc gag cgc atg ggg cac atg ctg cag cgg ccg ctg gtg ctg cac acg 864
95 Val Glu Arg Met Gly His Met Leu Gln Arg Pro Leu Val Leu His Thr
96                      275                      280                      285
98 tct gcg gcg gcc gag ctc ccc cgc gcc aac aca cac ata 903
99 Ser Ala Ala Ala Glu Leu Pro Arg Ala Asn Thr His Ile
100                      290                      295                      300
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 301
105 <212> TYPE: PRT
106 <213> ORGANISM: Ashbya gossipii
108 <400> SEQUENCE: 2
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110 1 5 10 15
112 Ile Pro Thr Val Gln Gly Thr Asp Val Phe Leu His Leu Tyr His Asn
113 20 25 30
115 Ser Ile Asp Ser Lys Glu His Leu Ala Ile Val Phe Gly Glu Asn Ile
116 35 40 45
118 Arg Ser Arg Ser Leu Phe Arg Tyr Arg Lys Asp Asp Thr Gln Gln Ala
119 50 55 60
121 Arg Met Val Arg Gly Ala Tyr Val Gly Gln Leu Tyr Pro Gly Arg Thr
122 65 70 75 80
124 Glu Ala Asp Ala Asp Arg Arg Gln Gly Leu Glu Leu Arg Phe Asp Glu
125 85 90 95
127 Thr Gly Gln Leu Val Val Glu Arg Ala Thr Thr Trp Thr Arg Glu Pro
128 100 105 110
130 Thr Leu Val Arg Leu His Ser Glu Cys Tyr Thr Gly Glu Thr Ala Trp

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131          115          120          125
133 Ser Ala Arg Cys Asp Cys Gly Glu Gln Phe Asp Gln Ala Gly Lys Leu
134          130          135          140
136 Met Ala Ala Ala Thr Glu Gly Glu Val Val Gly Gly Ala Gly His Gly
137 145          150          155          160
139 Val Ile Val Tyr Leu Arg Gln Glu Gly Arg Gly Ile Gly Leu Gly Glu
140          165          170          175
142 Lys Leu Lys Ala Tyr Asn Leu Gln Asp Leu Gly Ala Asp Thr Val Gln
143          180          185          190
145 Ala Asn Glu Leu Leu Asn His Pro Ala Asp Ala Arg Asp Phe Ser Leu
146          195          200          205
148 Gly Arg Ala Ile Leu Leu Asp Leu Gly Ile Glu Asp Ile Arg Leu Leu
149          210          215          220
151 Thr Asn Asn Pro Asp Lys Val Gln Gln Val His Cys Pro Pro Ala Leu
152 225          230          235          240
154 Arg Cys Ile Glu Arg Val Pro Met Val Pro Leu Ser Trp Thr Gln Pro
155          245          250          255
157 Thr Gln Gly Val Arg Ser Arg Glu Leu Asp Gly Tyr Leu Arg Ala Lys
158          260          265          270
160 Val Glu Arg Met Gly His Met Leu Gln Arg Pro Leu Val Leu His Thr
161          275          280          285
163 Ser Ala Ala Ala Glu Leu Pro Arg Ala Asn Thr His Ile
164          290          295          300
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 2528
170 <212> TYPE: DNA
171 <213> ORGANISM: Ashbya gossipii
173 <400> SEQUENCE: 3
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175 atgtccacat ccaccacgat cagctccgac gtcaccgtgt ggtccaccac cttgctcttg 120
176 acgctcacca gcgcctcgct cccgtcgctg gtaattatcc gcgcagaccc gtttgagtta 180
177 ggtaagaaat caaccgccac atccaagggg cggaactgcg ctgccgcccg cccgtctgcg 240
178 cgaatcggtg gtatcgctt cagtgaatca atcagataca gctgctcggt cactgatagc 300
179 atcatggcta atttctgtcc gcatacttca tatgctcatc gcacattgat aatgtacatt 360
180 cgaaaaatth caagattagc ctccgtgaac agcgatttac cttaggcaaa agtaacaaaa 420
181 ggcttttccg taggtgcttt gtcattcaac aatccacgtc ggaattggcg actatatagt 480
182 gtagggccca taaagcagta gtcgggtgtt atagctgtgt cagaccaact ctttgtaaat 540
183 tactgaagct gatatgactg aatacacagt gccagaagtg acctgtgtcg cacgcgcgcg 600
184 cataccgacg gtacagggca ccgatgtctt cctccatcta taccacaact cgatcgacag 660
185 caaggaacac ctagcgattg tcttcggcga gaacatacgc tcgcggagtc tgttccggta 720
186 ccggaagac gacacgcagc aggcgcgat ggtgcggggc gcctacgtgg gccagctgta 780
187 ccccgggcgg accgaggcag acgcggatcg gcgtcagggc ctggagctgc ggtttgatga 840
188 gacagggcag ctggtggtgg agcgggcgac gacgtggacc agggagccga cactggtgcg 900
189 gctgcactcg gagtgttaca cgggcgagac ggcgtggagc gcgcggtgcg actgcgggga 960
190 gcagttcgac caggcgggta agctgatggc tgcggcgaca gagggcgagg tggttggcgg 1020
191 tcgggggcac ggcgtgatcg tgtacctgcg gcaggagggc cgcgcatcg ggctaggcga 1080
192 gaagctgaag gcgtacaacc tgcaggacct gggcgcgagc acggtgcagg cgaacgagct 1140
193 gctcaaccac cctgcggacg cgcgcgactt ctcgttgggg cgcgcaatcc tactggacct 1200
194 cggtatcgag gacatccggt tgctcacgaa taaccccgac aaggtgcagc aggtgcaact 1260

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195 tccgccggcg ctacgctgca tcgagcgggt gcccatgggtg ccgctttcat ggactcagcc 1320
196 cacacagggc gtgcgctcgc gcgagctgga cggctacctg cgcgccaaagg tcgagcgcat 1380
197 gggggcacatg ctgcagcggc cgctgggtgct gcacacgtct cgggcggccg agctcccccg 1440
198 cgccaacaca cacatataat ctttgctata ttaaaactct ataaacgtat gccacacggc 1500
199 gcccgcgggc tgccacacgc tgctcacggg ctgccgaaca gttctaacaa gtaatcgcg 1560
200 gcctcgccag tgatcgtggc gagcaccttg tcgtccatca tcacatatcc tcggctacag 1620
201 tcgtcgttga agagcgctga cgtgcgcttc gacttggtgcg atttaaggaa gtcgttgat 1680
202 ccgttgaccg tggtagctc gaccggcgcg ctaacgagaa acgatcctgt ggaaccctgt 1740
203 gactcggacg actggaattg cgattggttc ttaagcttgt atagggtctg catcttctgt 1800
204 gttcagcttg gggatcgcg acggttttgc caccacgggt ctagtagtcg catttatata 1860
205 ctacggtact agccgcccct agctgggtccc gggaggggga gcgtcgccat cggttacggg 1920
206 tcacgtgggt ttgggtcgaag gcaatcgaag cgtcagggga gattctatgt gatgtctggg 1980
207 tatttgtagc gctgacgcac gtgactggcg gcataagtgt cagcacgcca gacgtgacgc 2040
208 gagccgcacg agccgtgcgg cactgactgc tgcgattggc gcgcatctca accacggatg 2100
209 aggggtccgc ttatggtcat gagcttagta aacttctgat tatattaag aatcatactc 2160
210 atataacatt caacgatata tcattctatt taaccactca agaataaacc tctaagtata 2220
211 ttacagaggt catatacata ttagattata caacagatta gtgtatttct tatctcacgt 2280
212 ataaacaaat aagtagattg gaggattcat atcagatatt aatgtaagac tcatattaaa 2340
213 ttcttagttc cttacaagtt taaacttcta agtatattga agaggtcata cttgaattaa 2400
214 actatacgat agatgatact cttttctttc tcttcgatta tattaatatga ttagtatatt 2460
215 atatgccatt tgataaaatg attgatatat tacaatatta tctttaatat tttaataata 2520
216 acaaatat 2528

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219 <210> SEQ ID NO: 4

220 <211> LENGTH: 582

221 <212> TYPE: DNA

222 <213> ORGANISM: Fusarium graminearum

224 <220> FEATURE:

225 <221> NAME/KEY: CDS

226 <222> LOCATION: (1)..(582)

228 <400> SEQUENCE: 4

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229 act ctc ccg gag gtg gaa tgc atc gtt cgt gcc cgt atc ccc acg gtt 48
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231 1 5 10 15
233 gca gga acc gag atg ttc ttg cac ctg tac acc aac aat gtg gac aac 96
234 Ala Gly Thr Glu Met Phe Leu His Leu Tyr Thr Asn Asn Val Asp Asn
235 20 25 30
237 aag gag cac ctc gcc atc gtg ttt ggc aaa aat atc cga agc aag agt 144
238 Lys Glu His Leu Ala Ile Val Phe Gly Lys Asn Ile Arg Ser Lys Ser
239 35 40 45
241 cta gat gct gtc cgg gag ggt gag acc gag atg gac cgc atg gtg cgc 192
242 Leu Asp Ala Val Arg Glu Gly Glu Thr Glu Met Asp Arg Met Val Arg
243 50 55 60
245 ggc gca tac aca gga agg ctg ttc ccc ggt cgc aca acc agt ggc atc 240
246 Gly Ala Tyr Thr Gly Arg Leu Phe Pro Gly Arg Thr Thr Ser Gly Ile
247 65 70 75 80
249 ggt cca gcg acc cct cag gag gaa cag cca ccg cag ccg tcg gat gag 288
250 Gly Pro Ala Thr Pro Gln Glu Glu Gln Pro Pro Gln Pro Ser Asp Glu
251 85 90 95
253 cct cct ctg gtg agg att cat tcc gag tgc tac aca ggt gag acg gcg 336

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254 Pro Pro Leu Val Arg Ile His Ser Glu Cys Tyr Thr Gly Glu Thr Ala
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257 tgg tca gcg cga tgc gac tgc ggc gag cag ctc gat gaa gca gcg cgc 384
258 Trp Ser Ala Arg Cys Asp Cys Gly Glu Gln Leu Asp Glu Ala Ala Arg
259      115      120      125
261 ctg atg agt ctg cca ggc aac aag gcc ggc ggc atc atc atc tac ctg 432
262 Leu Met Ser Leu Pro Gly Asn Lys Ala Gly Gly Ile Ile Ile Tyr Leu
263      130      135      140
265 cga caa gag ggt cgt ggt atc ggt ctg gga gag aag ctc aag gcg tac 480
266 Arg Gln Glu Gly Arg Gly Ile Gly Leu Gly Glu Lys Leu Lys Ala Tyr
267 145      150      155      160
269 aat ctt cag gat ctg ggg tct gat act gtc gag gcg aat ttg ctt ttg 528
270 Asn Leu Gln Asp Leu Gly Ser Asp Thr Val Glu Ala Asn Leu Leu Leu
271      165      170      175
273 cgc cat cct gcc gat gct cga agc tac ggt ctt gct acc gct atg ctg 576
274 Arg His Pro Ala Asp Ala Arg Ser Tyr Gly Leu Ala Thr Ala Met Leu
275      180      185      190
277 ctg gat 582
278 Leu Asp
281 <210> SEQ ID NO: 5
282 <211> LENGTH: 194
283 <212> TYPE: PRT
284 <213> ORGANISM: Fusarium graminearum
286 <400> SEQUENCE: 5
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288 1 5 10 15
290 Ala Gly Thr Glu Met Phe Leu His Leu Tyr Thr Asn Asn Val Asp Asn
291 20 25 30
293 Lys Glu His Leu Ala Ile Val Phe Gly Lys Asn Ile Arg Ser Lys Ser
294 35 40 45
296 Leu Asp Ala Val Arg Glu Gly Glu Thr Glu Met Asp Arg Met Val Arg
297 50 55 60
299 Gly Ala Tyr Thr Gly Arg Leu Phe Pro Gly Arg Thr Thr Ser Gly Ile
300 65 70 75 80
302 Gly Pro Ala Thr Pro Gln Glu Glu Gln Pro Pro Gln Pro Ser Asp Glu
303 85 90 95
305 Pro Pro Leu Val Arg Ile His Ser Glu Cys Tyr Thr Gly Glu Thr Ala
306 100 105 110
308 Trp Ser Ala Arg Cys Asp Cys Gly Glu Gln Leu Asp Glu Ala Ala Arg
309 115 120 125
311 Leu Met Ser Leu Pro Gly Asn Lys Ala Gly Gly Ile Ile Ile Tyr Leu
312 130 135 140
314 Arg Gln Glu Gly Arg Gly Ile Gly Leu Gly Glu Lys Leu Lys Ala Tyr
315 145 150 155 160
317 Asn Leu Gln Asp Leu Gly Ser Asp Thr Val Glu Ala Asn Leu Leu Leu
318 165 170 175
320 Arg His Pro Ala Asp Ala Arg Ser Tyr Gly Leu Ala Thr Ala Met Leu
321 180 185 190
323 Leu Asp

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date